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RAW SEQUENCE LISTING   DATE: 12/14/2001
PATENT APPLICATION: US/09/824,551   TIME: 12:37:45

Input Set : A:\Ma280106.app
Output Set: N:\CRF3\12142001\I824551.raw

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 3 <110> APPLICANT: BATHE, BRIGITTE
 4        KREUTZER, CAROLINE
 5        MARX, ACHIM
 6        PFEFFERLE, WALTER
 8 <120> TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE
 9        LUXS GENE
11 <130> FILE REFERENCE: MAS/21123/280106
13 <140> CURRENT APPLICATION NUMBER: 09/824,551
14 <141> CURRENT FILING DATE: 2001-04-04
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1902
22 <212> TYPE: DNA
23 <213> ORGANISM: Corynebacterium glutamicum
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (342)..(1610)
28 <223> OTHER INFORMATION: luxS-Gen
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31 ggtaggagta aaaaacgcag gagggcgtcg aaaagcgttc gtctgtgccg taacccgtga 60
33 cgcgctggcc gttggtatcg gcgacccagt cggtgcccag gtaggggcat gcggtttgtg 120
35 cggtgcgttc gaccgcgggc atcgcgtcga tgggaaggcc gtcagtaatt acttccgggg 180
37 ctgcctcggt ggtggtctct ggggttgctt caggttccgc cggggtacaa gcggtgagca 240
39 tgatggaagc agcgaggata gtaggtaatg tacgacgcat gcagtcaagc ctagatcgtg 300
41 tgtcggaaac cggacgcaat gagctcgatg ttgaaaccct t gtg aag aag ggg aat 356
42                                             Met Lys Lys Gly Asn
43                                              1               5
45 caa ccg ggc gcg atg agc tat cgc aac agt atc cac att ttg aca gcc 404
46 Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile His Ile Leu Thr Ala
47                10              15                  20
49 tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc cgc ctg acg ctg ccg 452
50 Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro
51                25                  30                  35
53 atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg tgg ggt ttt ctg tac 500
54 Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val Trp Gly Phe Leu Tyr
55            40                  45                  50
57 ttc tat gga tca acc aaa cgc gta gat ttg agc cac ggc atg cag ctg 548
58 Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser His Gly Met Gln Leu
59        55                  60                  65
61 ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att ttt atg gtg ccg atc 596
62 Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Met Val Pro Ile
63 70                  75                  80                  85
65 gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg ttt ttc ctc tat cta 644
66 Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu
67                90                  95                  100
69 cag gtg atg cct gac gtg aga ggc att att gcg att ttg ggt gcg aca 692
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70 Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr
71              105               110               115
73 gcg att gcg att gcc agc cag tat tcc gtg ggg ttg acc ttt ggt ggt   740
74 Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly
75              120               125               130
77 gtg atg ggt ccg gtg gtc tct gcg atc gtg acc gtg gct att gat tac   788
78 Val Met Gly Pro Val Val Ser Ala Ile Val Thr Val Ala Ile Asp Tyr
79     135               140               145
81 gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa aag cag gaa ttg att   836
82 Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu Lys Gln Glu Leu Ile
83 150               155               160               165
85 gat cag ttg att gaa act cgc tcc cag ctg gcg gtg acg gaa cga aat   884
86 Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala Val Thr Glu Arg Asn
87                   170               175               180
89 gcg ggt att gct gcg gaa cgt caa cgt att gcg cat gaa att cat gac   932
90 Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala His Glu Ile His Asp
91              185               190               195
93 acg gtc gcc cag gga ctc tcc tcc att caa atg ctg ctg cat gtc tct   980
94 Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met Leu Leu His Val Ser
95              200               205               210
97 gaa cag gag att ctc gtt gct gag atg gaa gag aag cca aag gag gcg   1028
98 Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu Lys Pro Lys Glu Ala
99     215               220               225
101 atc gtg aag aag atg cgc ctt gcc cga caa aca gcc tcc gac aat ctc  1076
102 Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu
103 230               235               240               245
105 agt gag gct cgc gcg atg att gcg gcg ttg caa ccg gca gcg ctg tct  1124
106 Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser
107                   250               255               260
109 aaa acc tcc ttg gaa gca gca ctt cac cgc gtc aca gaa ccg ttg ttg  1172
110 Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val Thr Glu Pro Leu Leu
111              265               270               275
113 ggt att aat ttt gtg att tct gtc gac ggt gat gtt cgc caa ctg ccc  1220
114 Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp Val Arg Gln Leu Pro
115              280               285               290
117 atg aaa act gaa gcc acc ctt ctg cga att gct caa ggt gcg atc gga  1268
118 Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly
119     295               300               305
121 aat gtg gcg aaa cat tca gag gcg aaa aac tgc cac gtg aca cta acc  1316
122 Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys His Val Thr Leu Thr
123 310               315               320               325
125 tac gaa gac aca gaa gta cgc ctt gat gtg gtt gat gac ggt gtg ggt  1364
126 Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val Asp Asp Gly Val Gly
127                   330               335               340
129 ttt gag cct tcg gaa gtg tcc agt acc ccc gct ggc ctt ggc cat atc  1412
130 Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala Gly Leu Gly His Ile
131              345               350               355
133 ggc tta acc gca ttg cag cag cgt gcg atg gaa ttg cac ggc gaa gtt  1460
134 Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu Leu His Gly Glu Val
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135        360                    365                    370
137 ata gtg gaa tct gca tat ggg cag ggt act gcg gta tct gca gca ttg  1508
138 Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala Val Ser Ala Ala Leu
139        375                    380            385
141 ccg gtg gag cca cca gag ggg ttt gtc ggg gcg ccg gtt ttg gca gat  1556
142 Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala Pro Val Leu Ala Asp
143 390                    395            400                405
145 tcg gac tca agt gct aca ggc gag gtt gaa cta agt tct cca act gac  1604
146 Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu Ser Ser Pro Thr Asp
147               410                    415            420
149 gat gag taaggctaga ctaaagtacg attcatctgc tcatcgatac tcttgaaggc  1660
150 Asp Glu
152 gcattttcat tcgaaacgaa gtgcgccatt gggaaggacc tagttcaaac aatgattcgc 1720
154 gtgctgcttg ctgatgacca cgaaatcgtg aggctcggac tccgagctgt gctggaaagc 1780
156 gccgaggaca ttgaagtggt gggcgaagtc tccaccgccg aaggtgcggt gcaggcagcc 1840
158 caagaaggcg gaatcgacgt catcttgatg gacctccgat tcggccccgg cgtccaagga 1900
                                                                     1902
160 ac
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 423
165 <212> TYPE: PRT
166 <213> ORGANISM: Corynebacterium glutamicum
168 <400> SEQUENCE: 2
169 Met Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile
170  1             5                  10                  15
172 His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala
173            20                 25                  30
175 Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
176         35                 40                  45
178 Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
179      50                 55                  60
181 His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
182 65                 70                  75                  80
184 Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
185                 85                 90                  95
187 Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
188            100                105                 110
190 Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
191         115                120                 125
193 Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
194      130                135                 140
196 Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
197 145                150                155                 160
199 Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
200                165                170                 175
202 Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala
203            180                185                 190
205 His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
206         195                200                 205
208 Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu
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209     210                   215           220
211 Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
212 225                   230           235               240
214 Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln
215                   245           250               255
217 Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
218                   260           265               270
220 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
221             275           280               285
223 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
224         290           295               300
226 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
227 305                   310           315               320
229 His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
230                   325           330               335
232 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
233             340           345               350
235 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
236         355           360               365
238 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
239         370           375               380
241 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
242 385                   390           395               400
244 Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
245                   405           410               415
247 Ser Ser Pro Thr Asp Asp Glu
248             420
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252 <210> SEQ ID NO: 3
253 <211> LENGTH: 20
254 <212> TYPE: DNA
255 <213> ORGANISM: Corynebacterium glutamicum
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Primer luxS-int1
260 <400> SEQUENCE: 3
261 tcgtgaccgt ggctattgat   20
264 <210> SEQ ID NO: 4
265 <211> LENGTH: 20
266 <212> TYPE: DNA
267 <213> ORGANISM: Corynebacterium glutamicum
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Primer luxS-int2
272 <400> SEQUENCE: 4
273 cttgagcaat tcgcagaagg   20

VERIFICATION SUMMARY   DATE: 12/14/2001
PATENT APPLICATION: US/09/824,551   TIME: 12:37:46

Input Set : **A:\Ma280106.app**
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